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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/446,024	12/16/1999	FREDERIC BESEME	105045	1689

7590 01/31/2002

OLIFF & BERRIDGE
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EXAMINER
LEFFERS JR, GERALD G

ART UNIT	PAPER NUMBER
1636	14

DATE MAILED: 01/31/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/446,024	BESEME ET AL.	
	Examiner	Art Unit	
	Gerald G Leffers Jr.	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *09 November 2001* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-14 and 18-38* is/are pending in the application.

4a) Of the above claim(s) *13,14 and 37* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-12,18-36 and 38* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Pri rity under 35 U.S.C. §§ 119 and 120

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☒ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *4, 5* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Receipt is acknowledged of applicants' preliminary amendment, filed 5/29/01 as Paper No. 9, in which several claims were amended (claims 1-4, 7-14, 18-20) and new claims added (claims 21-38).

Receipt is also acknowledged of applicants' preliminary amendment, filed 11/9/01 as Paper No. 12, in which the specification was amended to include sequence identifiers and in which a new paper copy of the sequence listing, computer readable form and corresponding attorney's statement were submitted.

Election/Restrictions

Applicant's election with traverse of Group I (claims 1-12, 15-20, 21-36, 38), claims drawn toward nucleic acids of a human endogenous retroviral genome and methods of using the same for diagnosis, in Paper No. 9 is acknowledged. The traversal is on the ground(s) that the therapeutic composition of claim 20 has a common technical feature (i.e. nucleic acid sequence) with the nucleic acids and methods of Group I. This is not found persuasive because it is not necessarily true that the nucleic acids used in the methods of Group I will be found in the therapeutic composition of claim 20. Moreover, the therapeutic composition has technical features in addition to just the presence of a nucleic acid derived from a particular source (e.g. pharmaceutically acceptable carriers, synergistic compounds, etc.).

The requirement is still deemed proper and is therefore made FINAL.

Claims 1-14 and 18-38 are pending in this application, with claims 13-14 and 37 withdrawn from consideration as being drawn towards a nonelected invention.

Specification

This application does not contain an abstract of the disclosure as required by 37 CFR 1.72(b). An abstract on a separate sheet is required.

Claim Objections

Claims1-12, 18-36 and 38 are objected to because of the following informalities: many of these claims lack an article (e.g. The, A, etc.) at the beginning of the claim and are grammatically incorrect. Appropriate correction is required.

Claims 33-35 are objected to because of the following informalities: elements a), b), c) recited in the body of these claims are not completely enclosed by parentheses, making it somewhat unclear as to what parts of the dependent claim these elements correspond. It would be remedial to amend the claims to enclose the recited elements completely in parentheses. Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 11 and 28-30 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

Each of these claims appear to be limited to nucleic acid sequences for which there appears to be no prior art describing a nucleic acid comprising the exact same sequence and for

which a specific and substantial utility has been demonstrated. Therefore, for these sequences there appears to be no well-established utility. Moreover, the prior art does not appear to provide support for any of the asserted utilities for the claimed nucleic acids.

The specification teaches that the claimed sequences were obtained from cDNAs isolated from placenta or from a deduced genomic RNA sequence based upon alignment of several overlapping cDNAs (termed by applicants as HERV-W). This proposed genomic RNA sequence (SEQ ID NO: 11) is described as having several of the characteristics of retroviral genomic RNAs. There is no description of a single genomic clone comprising all of the deduced RNA sequences. It is unclear whether there exists in the human genome a single complete copy of the deduced RNA genome. Several elements of the deduced RNA sequence do appear to be expressed in placental cells and not in several other cell types. The specification teaches that the genomic distribution of the HERV-W sequences throughout the genome is complex, with hundreds of partial sequences scattered across several different chromosomes.

Asserted utilities for the claimed nucleic acids are several, including for example, use of the nucleic acid sequences as markers or probes for several diseases or disorders such as autoimmune disease or unsuccessful pregnancy. All of the asserted utilities are dependent upon the recited sequences actually being correlated with a particular disease or condition. However, the specification provides no convincing evidence that such specific (i.e. correlating to a specific condition) or substantial (i.e. not requiring additional experimentation to identify or confirm) utilities exist for the claimed nucleic acids. For example, the specification bases several of its asserted utilities upon the observation that other human endogenous retroviral nucleic acid sequences have some unspecified degree of correlation to disease or disorders. There is no

significant correlation, however, between the prior art endogenous retroviral sequences and the instant nucleic acids with regard to specific diseases or disorders, and the specification provides no convincing rational as to why one of skill in the art would expect the claimed nucleic acid sequences to be correlated to the same conditions or diseases as is exhibited by other non-related HERV elements. The specification also asserts that the claimed nucleic acids can be used to diagnose risk of a pathological pregnancy or risk of unsuccessful pregnancy based upon the observation that a few of the sequences comprised within the proposed HERV-W sequence are expressed somewhat specifically in the placenta. However, there is no convincing rational presented in the specification as to why the recited sequences should be associated with a problem pregnancy. For example, there is no comparison of expression of the nucleic acids of the invention in abnormal pregnancies to expression of the same sequences in normal pregnancies.

Given that there is no well-established utility for nucleic acids comprising the recited nucleotide sequences, and that there is no convincing support provided by the specification or prior art for any of the asserted utilities such that the asserted utilities can be considered specific and substantial, one of skill in the art would reasonably conclude that the recited nucleic acid sequences lack specific and substantial utility.

Claims 11 and 28-30 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-12, 15-20, 21-36, 38 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1-4 are vague and indefinite in that the metes and bounds of the phrase "nucleic material of the retroviral genomic type" are unclear. The phrase does not appear to be well defined by the specification. For example, how homologous to a reference retroviral nucleotide sequence does a given sequence have to be in order to qualify as a nucleic acid of the "retroviral type"? How much of a nucleic acid derived from a retroviral genome must be present in order for it to be of a "retroviral genomic type"? It would be remedial to amend the claim language to more clearly indicate what is intended by the recited limitation of "nucleic material of the retroviral genomic type".

Claims 1 and 7 are vague and indefinite in that the metes and bounds of the term "equivalent" when applied to a nucleic acid sequence are unclear. The concept of equivalent protein or nucleic acid sequences does not appear to be well defined in the specification. For example, how homologous to a given reference sequence does a sequence have to be in order to qualify as an "equivalent" sequence to the reference? How much functional similarity for an encoded polypeptide to a reference polypeptide must there be in order for the nucleic or amino acid sequences to qualify as "equivalent"? It would be remedial to amend the claim language to explicitly define what is intended by the term "equivalent".

Claim 1 is also vague and indefinite in that it is unclear what is intended by the term "reference nucleotide sequence". This term does not appear to be well defined in the specification. It would be remedial to amend the claim language to clearly indicate what is intended by the recited term.

Claim 2 is vague and indefinite in that the metes and bounds of the phrase "capable of being encoded by at least a functional part of a reference nucleotide sequence" are unclear. Under what conditions is the peptide to be "capable of" being encoded by the recited sequences? Also, what exactly constitutes a "functional part" of a reference sequence? This term does not appear to be clearly defined in the specification.

Claims 3, 12 and 27 are vague and indefinite in that the metes and bounds of the term "fragment" are unclear in light of the claimed invention. What are the limits of a nucleic acid "fragment" in context of the claims? Would a single nucleic acid inserted, as specified in claims 3 and 27, between an LTR and gag gene constitute a "fragment"? From what source is the fragment to be derived? It would be remedial to amend the claim language to clearly indicate what is intended by the recited phrase.

Claim 7 is vague and indefinite in that the metes and bounds of the phrase "partial and complete" are unclear. For example, what constitutes a "complete" nucleic acid sequence according to claim 1? What constitutes a "partial" nucleic acid sequence of one of the recited clones? Would a single nucleotide satisfy this limitation?

Claim 8 is vague and indefinite in that the metes and bounds of the phrase "capable of hybridizing specifically" are unclear? Under what conditions is the hybridization to be

performed? How specific is "specific hybridization"? It would be remedial to amend the claim to include the hybridization conditions and the limits of "specific hybridization".

Claim 9 is vague and indefinite in that it is not clear what exactly constitutes a "marker" in the context of the claim. Does the term refer to a genetic marker or to some sort of label attached to the probe? Upon reading the specification, it appears the term is intended to specify some sort of label. It would be remedial to amend the claim language accordingly.

Claim 10 is vague and indefinite in that the metes and bounds of the phrase "capable of hybridizing" are unclear? Under what conditions is the hybridization to be performed? It would be remedial to amend the claim to include the hybridization conditions.

Claim 12 is vague and indefinite in that there is no clear and positive prior antecedent basis for the term "nucleotide fragment" in claim 7, upon which claim 12 is dependent.

Claim 18 is vague and indefinite in that the metes and bounds of the term "and/or" are inherently indefinite, making it unclear as to which combinations of limitations are acceptable.

Claim 20 is vague and indefinite in that the claim is drawn towards a non-elected embodiment (i.e. a therapeutic composition). It would be remedial to amend the claim language to delete this limitation.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

> (e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) do not apply to the examination of this application as the application being examined was not (1) filed on or after November 29, 2000, or (2) voluntarily published under 35 U.S.C. 122(b). Therefore, this application is examined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

Claims 1-10, 12, 18-36 and 38 are rejected under 35 U.S.C. 102(e) as being anticipated by Perron et al (U.S. Patent No. 6,001,987; see the entire document).

The Perron et al patent teaches the identification of sequences derived from a human endogenous retroviral genome and co-infective agent (MSVR-1 and MSVR-2, respectively) and which are associated with multiple sclerosis (MS), a disease with an autoimmune component (e.g. Abstract; column 3, lines 5-30; column 4, lines 15-50). The specification of the '987 patent teaches that the nucleic acids of the invention can be used for detection of a pathogenic and/or infective agent associated with MS (e.g. column 5, lines 10-29). The specification of the '987 patent teaches examples wherein specific MSRV-1 or MSRV-2 sequences are detected in samples (e.g. plasma or blood) obtained from patients having MS (e.g. Example 6).

The attached Sequence Identity search demonstrates that the sequence described by SEQ ID NO: 11 of the instant specification has 78.4% similarity to SEQ ID NO: 57 of the '987 patent. SEQ ID NO: 11 also has 88% similarity to SEQ ID NO: 89 of the '987 patent and 86.4% similarity to SEQ ID NO: 61 of the '987 patent. Figure 1 of the instant specification teaches that

SEQ ID NOS: 1-5, 7-10 are comprised within the proposed genomic RNA sequence described by SEQ ID NO: 11. The search report demonstrates several sequences which have very high identity with SEQ ID NO: 11. For example, from nt 2317 to nt 2438 of SEQ ID NO: 89 of the '987 patent, approximately 100 contiguous monomers, there is ~95% identity to SEQ ID NO: 11 of the instant specification.

Claims 1-9, 11-12, 24-27 and 31-36 are rejected under 35 U.S.C. 102(b) as being anticipated by Pauly or Waterston (Search Report #1, result # 3, Accession No. AC000064; available to the public since 13 November 1996).

As shown in the attached search report, Pauly and Waterston submitted the sequence of a human BAC clone, RG083M05. This sequence was available to the public as of 13 November 1996. Applicants admit in their specification that this genomic clone was available in the art at the time of applicants' invention and that the putative genomic RNA sequence has ~96% identity over its length with the sequence of RG083M05 (e.g. Example 2). The entire nucleotide sequence of RG083M05 can be used as a probe capable of hybridizing to SEQ ID NO: 11. Nucleic acid sequences within the BAC clone can be considered as "markers" for detection.

Conclusion

Claims 1-14, 18-38 are pending. Claims 13-14 and 37 are withdrawn from consideration as being directed towards a nonelected invention. No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gerald G Leffers Jr. whose telephone number is (703) 308-6232. The examiner can normally be reached on 9:30am-6:00pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached on (703) 305-1998. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 305-7939 for regular communications and (703) 305-7939 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

Gerald G Leffers Jr.
Examiner
Art Unit 1636

ggl
January 28, 2002

DAVID GUZO
PRIMARY EXAMINER

Attach To Paper No. 14

L Number	Hits	Search Text	DB	Time stamp
1	25	beseme-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:11
7	53	blond-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:11
13	203	bouton-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
19	119	mandrand-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
25	323	mallet-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
31	618	perron-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
37	1	beseme-$.in. and blond-$.in. and bouton-$.in. and mandrand-$.in. and mallet-$.in. and perron-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
43	1245	beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:13
49	0	(beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.) and (herv-w)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:13
55	27	(beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.) and ((herv-$2) or (endogenous adj4 retrovir$4))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:19
61	323	((herv-$2) or (endogenous adj4 retrovir$4))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:19
67	30	((herv-$2) or (endogenous adj4 retrovir$4)).ti.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:19
73	11	((herv-$2) or (endogenous adj4 retrovir$4)).clm.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:20
79	39	(((herv-$2) or (endogenous adj4 retrovir$4)).ti.) or (((herv-$2) or (endogenous adj4 retrovir$4)).clm.)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:20
85	35	((((herv-$2) or (endogenous adj4 retrovir$4)).ti.) or (((herv-$2) or (endogenous adj4 retrovir$4)).clm.)) not ((beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.) and ((herv-$2) or (endogenous adj4 retrovir$4)))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:20

(FILE 'HOME' ENTERED AT 08:47:47 ON 28 JAN 2002)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 08:48:08 ON 28 JAN 2002

L1	60	S (BESEME, ?)/IN,AU
L2	863	S (BLOND, ?)/IN,AU
L3	455	S (MANDRAND, ?)/IN,AU
L4	5300	S (MALLET, ?)/IN,AU
L5	1773	S (PERRON, ?)/IN,AU
L6	8	S L1 AND L2 AND L3 AND L4 AND L5
L7	2	DUPLICATE REMOVE L6 (6 DUPLICATES REMOVED)
L8	8268	S L1 OR L2 OR L3 OR L4 OR L5
L9	40	S L8 AND HERV-W
L10	14	DUPLICATE REMOVE L9 (26 DUPLICATES REMOVED)
L11	13	S L10 NOT L6
L12	3	S L8 AND HERV-H
L13	1	DUPLICATE REMOVE L12 (2 DUPLICATES REMOVED)
L14	3520	S HUMAN (S) ENDOGENOUS (S) RETROVIR?
L15	3497	S L14 NOT (L6 OR L9 OR L12)
L16	260	S L15 AND (PLACENTA OR PREGN?)
L17	8	S L16 AND HERV-H
L18	2	DUPLICATE REMOVE L17 (6 DUPLICATES REMOVED)
L19	14	S L16 AND HERV-W
L20	5	DUPLICATE REMOVE L19 (9 DUPLICATES REMOVED)

Access DB# 48622

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Gerald G Leffers Jr. Examiner #: 77472 Date: 8-8-01
Art Unit: 1636 Phone Number 308-6232 Serial Number: 09/446,024 wfe
Mail Box and Bldg/Room Location: [redacted] Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

***For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.**

Please Search SEQ ID #11-15

- Some Claims to any 100 contiguous NT's from SEQ ID #11-15

Point of Contact:
Susan Hanley
Technical Info. Specialist
CM1 12C14 Tel: 305-4053

I approve

RECEIVED
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new 11-15

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Searcher: Hanley
Searcher Phone #: _____
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Date Searcher Picked Up: 8/10
Date Completed: 8/16
Searcher Prep & Review Time: 10
Clerical Prep Time: 8
Online Time: 10

Type of Search

NA Sequence (#) 5
AA Sequence (#) _____
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr.Link _____
Lexis/Nexis _____
Sequence Systems _____
WWW/Internet _____
Other (specify) _____

PTO-1590 (1-2000)

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 15, 2001, 11:11:46 ; Search time 20850.3 Seconds
(without alignments)
5624.693 Million cell updates/sec

Title: US-09-446-024-11
Perfect score: 7582
Sequence: 1 caacaatcgggatataaacc.....tattaaatcttgcarctgcr 7582

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		7489.6	98.8	7582	9	AX000966	AX000966 Sequence
2		7489.6	98.8	7582	9	AX027480	AX027480 Sequence
3		6448	85.0	56093	93	HSAC000064	AC000064 Human BAC
c 4		6448	85.0	149194	86	AC007566	AC007566 Homo sapi
5		6436	84.9	10499	9	AX007980	AX007980 Sequence
c 6		5824.2	76.8	158053	65	AC018926	AC018926 Homo sapi
c 7		5492	72.4	193159	61	AC009727	AC009727 Homo sapi
8		4302.2	56.7	114621	85	AC005187	AC005187 Homo sapi

```
Qy   6241 ggacctcttgtttccaatstggaaataacccatacctcaaacctcacctgtgtaaaattt 6300
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Db   6241 GGACCTCTTGTTTCCAATSTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 6300

Qy   6301 agcaatactacatacacaaccaactcccaatgcatcaggtgggtaactcctcccacacaa 6360
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Db   6301 AGCAATACTACATACACAACCAACTCCCAATGCATCAGGTGGGTAACTCCTCCCACACAA 6360

Qy   6361 atagtctgcctaccctcaggaatatttttttgtctgtggtacctcagcctatcgttgtttg 6420
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Db   6361 ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG 6420

Qy   6421 aatggctcttcagaatctatgtgcttcctctcattcttagtgccccyatgrccatctac 6480
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Db   6421 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCYATGRCCATCTAC 6480

Qy   6481 actgaacaagatttatacagttatgtcatatctaagccccgcaacaaaagagtacccatt 6540
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Db   6481 ACTGAACAAGATTTATACAGTTATGTCATATCTAAGCCCCGCAACAAAAGAGTACCCATT 6540

Qy   6541 cttccttttgttataggagcaggagtgctaggtgcactaggtactggcattggcggtatc 6600
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Qy   6601 acaacctctactcagttctactacaaactatctcaagaactaaatggggacatggaacgg 6660
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Db   6601 ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAACTAAATGGGGACATGGAACGG 6660

Qy   6661 gtcgccgactccctggtcaccttgcaagatcaacttaactccctagcagcagtagtcctt 6720
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Qy   6961 ctactcctctttggaccctgtatctttracctccttgttaactttgtctcttccagaatc 7020
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Qy   7081 cccctggaccggcctgytagcccacgatctgatgttaatgacatcaaaggcaccccctcct 7140
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Qy   7141 gaggaaatctcagctgcacaacctctactacgccccaattcagcaggaagcagttagagc 7200
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Qy   7201 ggtsgtcggccaacctccccaacagcacttaggttttcctgttgagatgggggactgaga 7260
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Db   7201 GGTSGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGA 7260

Qy   7261 gacaggactagctggatttcctaggctgaytaagaatccytaagcctagstgggaaggtg 7320
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Db   7261 GACAGGACTAGCTGGATTTCCTAGGCTGAYTAAGAATCCYTAAGCCTAGSTGGGAAGGTG 7320

Qy   7321 accacatccaccttaaacacggggcttgcaacttagytcacacctgaccaatcagagag 7380
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Qy   7381 ctcactaaaatgctaattaggcaaagacaggaggtaaagaaatagccaatci
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   7441 mtgagagcacagcaggagggacaatgatcgggatataaacccaagtyttcga
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Qy   7501 cggcaaccccctttgggtcccctcccctttgtatgggagctctgttttcatgctatttcac 7560
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Qy   7561 tctattaaatcttgcarctgcr 7582
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Db   7561 TCTATTAAATCTTGCARCTGCR 7582


RESULT   3
HSAC000064
LOCUS       HSAC000064  56093 bp    DNA             PRI       13-NOV-1996
DEFINITION  Human BAC clone RG083M05 from 7q21-7q22, complete sequence.
ACCESSION   AC000064
VERSION     AC000064.1  GI:1669369
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 56093)
  AUTHORS   Pauley,A.
  TITLE     The sequence of H. sapiens BAC clone RG083M05
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 56093)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-1996)
COMMENT       Genome Sequencing Center
              Department of Genetics, Washington University
              St. Louis, MO 63108, USA
              e-mail: sapiens@watson.wustl.edu

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            sections once, or longer because we provide a small overlap between
            neighboring submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded or sequenced with an alternate
            chemistry; an attempt was made to resolve all sequencing problems,
            such as compressions and repeats; all regions were covered by
            sequence from more than one subclone; and the assembly was
            confirmed by restriction digest.

            SOURCE INFORMATION:
            This clone is from the first release of the human BAC library.  The
            library contains cloned DNA from a human male fibroblast cell line
            978SK.  For references see:  Shizuya et al., Proc. Natl. Acad. Sci.
            89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
            VECTOR:  pBELO
            Selection:  chloramphenicol

            NEIGHBORING SEQUENCE INFORMATION:
            The orientation of this clone is unknown.  Actual start of this
            clone is at base position 1 of H_RG083M05; actual end is at 56093
            of H_RG083M05

            This clone contains STS sWSS1725.
FEATURES              Location/Qualifiers
     source           1. .56093
                      /organism="Homo sapiens"
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                /chromosome="7"
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                /clone_lib="CITB-978SK-B"
                /map="7q21-7q22"
repeat_region   complement(838. .1131)
                /rpt_family="ALU"
gene            <1360. .16971
                /gene="WUGSC:H_RG083M05.1"
CDS             join(<1360. .1503,4181. .4370,4587. .4774,6422. .6556,
                9483. .9547,11631. .11773,11864. .12021,13131. .13296,
                14885. .14988,16349. .16546,16837. .16971)
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                /note="ATPase; strong similarity to peroxisome
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                /protein_id="AAB46346.1"
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                TIQLPAKVCLKKEKYPELFANLPIRQRTGILLYGPPGTGKTLLAGVIARESRMNFISV
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                LLTQLDGVEGLQGVYVLAATSRPDLIDPALLRPGRLDKCVYCPPPDQVTISYLESKTQ
                QMLHSFLVSRLEILNVLSDSLPLADDVDLQHVASVTDSFTGADLKALLYNAQLEALHG
                MLLSKMSEILPDESKFNMYRLYFGSSYESELGNGTSSDLSSQCLSAPSSMTQDLPGVP
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repeat_region   complement(6581. .7133)
                /rpt_family="L1"
repeat_region   complement(7767. .8037)
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repeat_region   complement(8186. .8472)
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misc_feature    8473. .8625
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misc_feature    8841. .9161
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                /note="match to human 5' EST H75921 (NID:g1050050), bases
                21-348"
misc_feature    9481. .9547
                /gene="WUGSC:H_RG083M05.1"
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                /note="match to human 5' EST H41382 (NID:917434), bases
                143-266"
repeat_region   13794. .13877
                /rpt_family="ALU"
misc_feature    13878. .13906
                /gene="WUGSC:H_RG083M05.1"
                /note="match to human 5' EST H41382 (NID:g917434), bases
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repeat_region   13907. .14104
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repeat_region   complement(14110. .14137)
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repeat_region   complement(15618. .15907)
                /rpt_family="ALU"
repeat_region   17227. .17522
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misc_feature    18667. .19235
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                (NID:g759399)"
repeat_region   19550. .19670
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misc_feature    21507. .37303
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exon            37316. .37489
                /note="Grail prediction, score = 80"
                /evidence=not_experimental
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misc_feature    39225. .39707
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repeat_region   39800. .40085
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misc_feature    complement(45614. .45737)
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repeat_region   complement(47027. .47318)
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misc_feature    complement(47365. .47782)
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misc_feature    47898. .48115
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repeat_region   complement(48116. .48405)
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misc_feature    complement(48406. .48584)
                /note="match to human 3' EST N29952 (NID:g1148472), bases
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repeat_region   complement(48787. .49405)
                /rpt_family="ALU"
misc_feature    complement(49406. .49534)
                /note="match to human 3' EST R65794 (NID:g838432), bases
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repeat_region   complement(49638. .49672)
                /rpt_family="ALU"
misc_feature    complement(49674. .49890)
                /note="match to human 3 ' EST N29952 (NID:g1148472) and 5'
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gene            complement(49698. .51806)
                /gene="WUGSC:H_RG083M05.2"
CDS             complement(join(49698. .49888,51575. .51806))
                /gene="WUGSC:H_RG083M05.2"
                /note="coded for by human cDNAs W37389 (NID:g1319205),
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exon            complement(51576. .51758)
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  Query Match           85.0%;  Score 6448;  DB 93;  Length 56093;
  Best Local Similarity  95.7%;  Pred. No. 0;
  Matches 6681;  Conservative  195;  Mismatches   50;  Indels   53;  Gaps   27;

Qy    606 gatgggaaacgttccccgcaagacaaaaacgccccctaagacgtattctggaraattggga 665
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Qy    666 mcaatttgaccctcagacactaagaaagaaacgacttatattcttctgcagtgccgcctg 725
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Qy    786 aaggcaaatggagtgaagtgccataagtacaaactttcttttcattaagagacaactcac 845
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Qy    846 aattatgtaaaaagtgtgatttatgccctacaggaagccttcagagtctacctccctatc 905
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Db  31193 AATTATGTAAAAAGTGTGATTTATGCCCTACAGGAAGCCTTCAGAGTCTACCTCCCTATC 31252

Qy    906 ccagcatccccgactccttcctcamytaataaggacccccccttcaacccaaatggtccaa 965
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Qy   1026 cccctcccaagcagtgggaggaagagaattcggcccagccagagtgcatgtgcytttyy 1085
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Db  31373 CCCCT-CCAAGCAGTGGGAGGAAGAGAATTCGGCCCAGCCAGAGTGCATGTGCCTTTTTC 31431

Qy   1086 tctcccagacttaaagcaaataaaaacagacttaggtaaattctcagataaycctgatgg 1145
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Qy   1146 ctatattgrtgttttacaagggttaggacaattctttgatctgacatggagagatatata 1205
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Db  31492 CTATATTGATGTTTTACAAGGGTTAGGACAATTCTTTGATCTGACATGGAGAGATATA-A 31550

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Db  31551 TGTCACTGCTAAATCAGACACTAACCCCAAATGAGAGAAGTGCCACCATAACTGCAGCCT 31610

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Db  31611 GAGAGTTTGGCGATCTCTGGTATCTCAGTCAGGTCAATG--ATAGGATGACAACAG-AGG 31667

Qy   1326 aaaganaatgattccccacaggccagcargcagttcccagtctasaccctcattggggac 1385
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Db  31668 AAAGAGAATGATTCCCCACAGGCCAGCAGGCAGTTCCCAGTCTAGACCCTCATTGGG--- 31724

Qy   1386 acagaaatcagtaacatgggagattggtgctgcagacatttgctaacttgtgtgctasaa 1445
          ||| | |     ||||| ||||||||||||||||||||||||||||||||||||:||
Db  31725 ACACAGAATCAGAACAT-GGAGATTGGTGCTGCAGACATTTGCTAACTTGTGTGCTAGAA 31783

Qy   1446 ggactaaggaaaactasgaagaaartctaygaattactcaatgatgtccaccataacaca 1505
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Db  31784 GGACTAAGGAAAACTAGGAAG-AAGTCTATGAATTACTCAATGATGTCCACCATAACACA 31842

Qy   1506 ggggaagggaagaaaatcctactgcctttctggagagactaagggaggcattgaggaagc 1565
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Db  31843 -GGGAAGGGAAGAAAATCCTACTGCCTTTCTGGAGAGACTAAGGGAGGCATTGAGGAAGC 31901

Qy   1566 gtgcctctctgtcacctgactcttctgaaggccaactaatcttaaagcgtaagtttatca 1625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31902 GTGCCTCTCTGTCACCTGACTCTTCTGAAGGCCAACTAATCTTAAAGCGTAAGTTTATCA 31961

Qy   1626 ctcagtcagctgcagacattag-aaaaaacttcaaaagtctgccgtaggcccggagcaaa 1684
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Db  31962 CTCAGTCAGCTGCAGACATTAGAAAAAAACTTCAAAAGTCTGCCGTAGGCCCGGAGCAAA 32021

Qy   1685 acttagaaaccctattgaacttggcaacytcggttttttataatagagatcaggaggagc 1744
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Qy   1745 aggcggaacaggacaaacgggattaaaaaaaaggccaccgctttagtcatgaccctcagg 1804
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Db  32082 AGGCGGAACAGGACAAACGGGATTAAAAAAAAGGCCACCGCTTTAGTCATGACCCTCAGG 32141

Qy   1805 caagtggactttggaggctctggaaaagggaaaagctgggcaaattgaatgcctaatagg 1864
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1865 gcttgcttccagtgcggtctacaaggacactttaaaaaagattgtccaagtagaagtaag 1924
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1925 ccgccccttcgtccatgccccttatttcaagggaatcactggaaggcccactgccccagg 1984
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32262 CCGCCCCCTCGTCCATGCCCCTTATTTCAAGGGAATCACTGGAAGGCCCACTGCCCCAGG 32321

Qy   1985 ggacaaaggtcttttgagtcagaagccactaaccagatgatccagcagcaggactgaggg 2044
          |||||||||| | ||||||||||||||||||||||||||||||||||||||||||||||
Db  32322 GGACAAAGGTCCTCTGAGTCAGAAGCCACTAACCAGATGATCCAGCAGCAGGACTGAGGG 32381

Qy   2045 tgcctggggcaagcgccatcccatgccatcaccctcacagagccctgggtatgcttgacc 2104
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32382 TGCCTGGGGCAAGCGCCATCCCATGCCATCACCCTCACAGAGCCCTGGGTATGCTTGACC 32441

Qy   2105 attgagggccaggaaggttgtctcctggacactggtgcggtcttcttagtcttactcttc 2164
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Db  32442 ATTGAGGGCCAGG-AGGTTGTCTCCTGGACACTGGTGCGGTCTTCTTAGTCTTACTCTTC 32500

Qy   2165 tgtcccggacaactgtcctccagatctgtcactattctgaggggtccntaagacgggca 2224
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Qy   2225 gtcactagatactttytcccagccactaagttatgaactggggagctttattcttttcac 2284
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Qy   2645 cacagaaacccagtggacagtggagggttagtgcaagatctcaggattatcaatggaggc 2704
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Db 32968 TACAGAAACCCAACAGACAGTGGA-GGTTAGTGCAAGATCTCAGGATTATCAAT-GAGGC 33025

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Qy   7504 caaccccctttgggtcccctcccttgtatgggagctctgttttcatgctatttcactct 7563
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RESULT   4
AC007566/c
LOCUS       AC007566   149194 bp    DNA                 PRI       16-NOV-2000
DEFINITION  Homo sapiens clone CTB-10G5, complete sequence.
ACCESSION   AC007566
VERSION     AC007566.2  GI:11181861
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 149194)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 149194)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 149194)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   4  (bases 1 to 149194)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            16, 2000 this sequence version replaced gi:4835815.
            ject name: H_RG010G05.

FEATURES
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ORIGIN


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  Matches 6681;  Conservative  195;  Mismatches   50;  Indels   53;  Gaps   27;

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ATTACHMENT: SEARCH REPORT #2 09/446,024 ATTACH TO PAPER #14

File Copy

GenCore version 4.5

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Run on: August 15, 2001, 11:11:46 ; Search time 285.92 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	932.4	12.3	1158	1	US-08-471-724-1	Sequence 1, Appli
	5	932.4	12.3	1158	2	US-08-471-969-1	Sequence 1, Appli
	6	932.4	12.3	1158	2	US-08-384-137-1	Sequence 1, Appli
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	10	644.4	8.5	2448	3	US-08-691-563C-53	Sequence 53, Appl
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ALIGNMENTS

RESULT 1
US-08-691-563C-57
; Sequence 57, Application US/08691563C
; Patent No. 6001987
; GENERAL INFORMATION:
; APPLICANT: Herve PERRON
; APPLICANT: Frederic BESEME
; APPLICANT: Frederic BEDIN
; APPLICANT: Glaucia PARANHOS-BACCALA
; APPLICANT: Florence KOMURIAN-PRADEL
; APPLICANT: Colette JOLIVET
; APPLICANT: Bernard MANDRAND
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
; TITLE OF INVENTION: THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,563C
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2391 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-691-563C-57

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RESULT   2
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; Sequence 89, Application US/08691563C
; Patent No. 6001987
  GENERAL INFORMATION:
    APPLICANT:  Herve PERRON
    APPLICANT:  Frederic BESEME
;   APPLICANT:  Frederic BEDIN
;   APPLICANT:  Glaucia PARANHOS-BACCALA
;   APPLICANT:  Florence KOMURIAN-PRADEL
;   APPLICANT:  Colette JOLIVET
;   APPLICANT:  Bernard MANDRAND
;   TITLE OF INVENTION:  VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
;   TITLE OF INVENTION:  ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
;   TITLE OF INVENTION:  THERAPEUTIC PURPOSES
;   NUMBER OF SEQUENCES:  92
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Oliff & Berridge
;     STREET:  700 South Washington Street, Suite 300
;     CITY:  Alexandria
;     STATE:  Virginia
;     COUNTRY:  U.S.A.
;     ZIP:  22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/691,563C
;     FILING DATE:  02-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Berridge, William P.
      REGISTRATION NUMBER:  30,024
      REFERENCE/DOCKET NUMBER:  WPB 38588
    TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-836-6400
;     TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  89:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1577 base pairs
;     TYPE:  nucleotide
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
US-08-691-563C-89


  Query Match           14.1%;  Score 1069.4;  DB 3;  Length 1577;
  Best Local Similarity   88.0%;  Pred. No. 0;
  Matches 1288;  Conservative   39;  Mismatches  111;  Indels   26;  Gaps   15;

Qy   1801 caggcaagtggactttggaggctctggaaaagggaaaagctgggcaaattgaatgcctaa 1860
          |||||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||||
Db    137 CAGGCAAGTGGACATTGGAGGCTCTGGAAAAGGGAAAAGTTGGGCAAATTGAATGCCTAA 196

Qy   1861 tagggcttgcttccagtgcggtctacaaggacactttaaaaaagattgtccaagtagaag 1920
          ||||||||||||||||| |||||||||||| ||||| ||||||||||||||||||||
Db    197 TAGGGCTTGCTTCCAGTGCAGTCTACAAGGACGCTTTAGAAAAGATTGTCCAAGTAGAAA 256

Qy   1921 taagccgccccttcgtccatgccccttatttcaagggaatcactggaaggcccactgccc 1980
          |||||||||||| |||||||||||||||||| ||||||||||||||||||||||| |||||||
Db    257 TAAGCCGCCCC-TCGTCCATGCCCCTTATGTCAAGGGAATCACTGGAAGGCCTACTGCCC 315

Qy   1981 caggggacaaaggtcttttgagtcagaagccactaaccagatgatccagcagcaggactg 2040
          |||||||| |||||| | ||||||||||||||||||||| ||||||||||||||||||||
Db    316 CAGGGGACGAAGGTCCTCTGAGTCAGAAGCCACTAACCTGATGATCCAGCAGCAGGACTG 375

Qy   2041 agggtgcctggggcaagcgccatcccatgccatcaccctcacagagccctgggtatgctt 2100
          |||||||| |||||||| |||| |||||||||||||||  |||||||| ||||||| ||
Db    376 AGGGTGCCCGGGGCAAGTGCCAGCCCATGCCATCACCCT--CAGAGCCCCGGGTATGTTT 433

Qy   2101 gaccattgagggccaggaaggt---tgtctcctggacactggtgcggtcttcttagtctt 2157
          |||||||||| |||||||||  |   |||||||||||||||| || | ||||| ||||||
Db    434 GACCATTGAGAGCCAGGAAGTTAACTGTCTCCTGGACACTGGCGCAGCCTTCTCAGTCTT 493

Qy   2158 actcttctgtcccggacaactgtcctccagatctgtcactattctgaggggtccntaag 2217
          ||| | ||||||| ||||| |||||||||||||||||||||| |   | |||  | ||||
Db    494 ACTTTCCTGTCCCAGACAATTGTCCTCCAGATCTGTCACTATCC---GAGGGGTCCTAAG 550

Qy   2218 acgggcagtcactagatactttytcccagccactaagttatgaactggggagctttattc 2277
          || | ||||||||| |||| ||:|| |||||||||||||| || |||||||| ||||| ||
Db    551 ACAGCCAGTCACTACATAC-TTCTCTCAGCCACTAAGTTGTG-ACTGGGGAACTTTACTC 608

Qy   2278 ttttcacatgcttttctaattatgcttgaaagccccactaccttgttagggagagacatt 2337
          |||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||
Db    609 TTTTCACATGCTTTTCTAATTATGCCTGAAAGCCCCACTCCCTTGTTAGGGAGAGACATT 668

Qy   2338 ctagcaaaagcaggggccattatacacctgaacataggagaaggaacacccgtttgttgt 2397
          |||||||||||||||||||||||||||||||||||||||||||| |||||| |||| |||
Db    669 TTAGCAAAAGCAGGGGCCATTATACACCTGAACATAGGAAAAGGAATACCCATTTGCTGT 728

Qy   2398 nccccctgcttgaggaaggaattaatcctgaagtctgggcaacagaaggacaatatggacg 2457
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 -CCCCTGCTTGAGGAAGGAATTAATCCTGAAGTCTGGGCAATAGAAGGACAATATGGACA 787

Qy   2458 agccaaagaatgcccgtcctgttcaagttaaactaaaggattccacttcctttccctacc 2517
          || |||||||||||||||||||||||||||||||||||||||  | ||||||||||||||
Db    788 AG-CAAAGAATGCCCGTCCTGTTCAAGTTAAACTAAAGGATTCTGCCTCCTTTCCCTACC 846

Qy   2518 aaaggcagtacccccctcagacccaaggcccaacaaggattccaaaagattgttaaggact 2577
          ||||| ||||||| || |||||| |||||| ||||||| | ||||||||||||||||||
Db    847 AAAGGAAGTACCCTCTTAGACCCGAGGCCCTACAAGGACT-CAAAAGATTGTTAAGGACC 905

Qy   2578 taaaagcccaaggcttagtaaaaccatgcataactccctgcagtaattccgtagtggatt 2637
          |||||||||||||| ||||||||||||||  | ||||||| || | |        |||
Db    906 TAAAAGCCCAAGGCCTAGTAAAACCATGCAGTAGCCCCTGCAATACTCC-------AATT 958

Qy   2638 gaggaggcacagaaacccagtggacagtggagggttagtgcaagatctcaggattatcaa 2697
          |  | |  |||||||| |||||||||| |||||||||||||||||||||||||||| ||
Db    959 TTAGGAGTAAGGAAACCCAACGGACAGTGGA-GGTTAGTGCAAGATCTCAGGATTATTAA 1017

Qy   2698 tggaggccgttgtccttttatacccagctgtacctagcccttatactgtgmyttcccaaa 2757
          | ||||| ||| | | | |||||||||||||| |||||||||||||| ||:::|||||| ||
Db   1018 T-GAGGCTGTTTTTCCTCTATACCCAGCTGTATCTAGCCCTTATACTCTGCTTTCCCTAA 1076

Qy   2758 taccagaggaagcagagtggtttacastcctggaccttmaggatgccttcttctgcatcc 2817
          |||||||||||||||||| |||||||:|||||||||||:|||||||||  ||||||||||
Db   1077 TACCAGAGGAAGCAGAGTAGTTTACAGTCCTGGACCTTAAGGATGCCTCTTTCTGCATCC 1136

Qy   2818 ctgtacatcctgactctcaattcttgtttgcctttgaagatacttcaaacccarcatctc 2877
          |||||||||||||| |||||||||||||||| |||||||||| |||  |||||||:  ||||
Db   1137 CTGTACATCCTGATTCTCAATTCTTGTTTGTCTTTGAAGATCCTTTGAACCCAATGTCTC 1196

Qy   2878 aactcacctggactrttttaccccaagggttcagggatagyccccatctatttggccagg 2937
          || |||||||||||:|||||||||| |||||| |||||||:|||||||||||||||||||
Db   1197 AATTCACCTGGACTGTTTTACCCCAGGGGTTCCGGGATAGCCCCCATCTATTTGGCCAGG 1256

Qy   2938 cattagcccaagacttgagycartymtcatacctggacactcttgtccttcrgtakgtgg 2997
          ||||||||||||||||||:||:|::|||||||||||||| ||||||||||:|||:| ||
Db   1257 CATTAGCCCAAGACTTGAGCCAATTCTCATACCTGGACA-TCTTGTCCTTCGGTATG-GG 1314

Qy   2998 atgatttacttttrgcygccyrttcagaaaccttgtgccatcaagccacccaagcrctct 3057
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Db   1315 ATGATTTAATTTTAGCCACCCGTTCAGAAACCTTGTGCCATCAAGCCACCCAAGCGTTCT 1374

Qy   3058 tmaatttcctcgcyacctgtggctacawggtttccaaacsarargctcarctctgctcac 3117

Db   1375 TAAATTTCCTCACTCCGTGTGGCTACAAGGTTTCCAAACCAAAGGCTCAGCTCTGCTCAC 1434

Qy   3118 agcaggttaaatacttaggrctaarattatccaaaggcaccarggccctcagtgaggaay 3177

Db   1435 AGCAGGTTAAATACTTAGGGTTAAAATTATCCAAAGGCACCAGGGCCCTCTGTGAGGAAT 1494

Qy   3178 ryatccagcctatactggcttatcctcatcycaaaaccctaaagcaactaagrgrrttcc 3237

Db   1495 GTATCCAACCTGTACTGGCTTATCTTCATCCCAAAACCCTAAAGCAACTAAGA-AGGTCC 1553

Qy   3238 ttggcrtaayaggyttctgccgaa 3261

     1554 TTGGCATAACAGGTTTCTGCCGAA 1577


RESULT   3
US-08-691-563C-61
; Sequence 61, Application US/08691563C
; Patent No. 6001987
;  GENERAL INFORMATION:
;    APPLICANT:  Herve PERRON
;    APPLICANT:  Frederic BESEME
;    APPLICANT:  Frederic BEDIN
;    APPLICANT:  Glaucia PARANHOS-BACCALA
;    APPLICANT:  Florence KOMURIAN-PRADEL
;    APPLICANT:  Colette JOLIVET
;    APPLICANT:  Bernard MANDRAND
;    TITLE OF INVENTION:  VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
;    TITLE OF INVENTION:  ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
;    TITLE OF INVENTION:  THERAPEUTIC PURPOSES
;    NUMBER OF SEQUENCES:  92
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oliff & Berridge
;      STREET:  700 South Washington Street, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/691,563C
;      FILING DATE:  02-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berridge, William P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6400
;      TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1167 base pairs
;      TYPE:  nucleotide
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-691-563C-61


  Query Match           12.5%;  Score 947.8;  DB 3;  Length 1167;
  Best Local Similarity  86.4%;  Pred. No. 2.7e-283;
  Matches 1013;  Conservative   77;  Mismatches   73;  Indels   10;  Gaps    6;

Qy   3313 aaggaaactcagaaagccaatacccatttartaagatggayamctgaagymraagtggct 3372

Db      1 AAGGAAACTCAGAAAGCCAATACCCATTTAGTAAGATGGACACCAGAAGCAGAAGCAGCT 60

Qy   3373 ttccaggcccctaaagaaggccttaaacccaagycccagtgttaagyttgccaacrgggc 3432

Db     61 TTCCAGGCCCTAAAGAAATCCCT--AACCCAAGCCCCAGTGTTAAGCTTGCCAACGGGGC 118

Qy   3433 aagacttttsttyatayrtcacagaaaaaaacagraayagctctrggagtccttacacag 3492

Db    119 AAGACTTTTCTTTATATGTCACAG--AAAAACAGGAATAGCTCTAGGAGTCCTTACACAG 176

Qy   3493 rtccragggaygagcttgcaaccyrtggcryacctgastaaggaaaytgatgtagtggca 3552

Db    177 GTCCAAGGGACAAGCTTGCAACCTGTGGCATACCTGAGTAAGGAAACTGATGTANTGGCA 236

Qy   3553 aagggttgrcytcattgtttaygggtagtggtggcagtagcagtyktagtatctgaagca 3612

Db    237 AAGGGTTGGCCTCATTGTTTACAGGTAG-GGCAGCAGTAGCAGTCTTAGTTTCTGAAACA 295

Qy   3613 gttaaaataatacagggragagatcttactgtgtggacatctcatgakgtgaayrgcata 3672

Db    296 GTTAAAATAATACAGGGAAGAGATCTTACTGTGTGGACATCTCATGATGTGAACGGCATA 355

Qy   3673 ctcactgctaaaggagacttgtggctgtcagacaacygtttacttaaatrtcaggctcta 3732

Db    356 CTCACTGCTAAAGAGGACTTGTGGCTGTCAGACAACCATTTACTTAAATAGCAGGTTCTA 415

Qy   3733 ttacttgaarggccagtgctgcractgtgcacttgtgcaactcttaacccagycncattt 3792

Db    416 TTACTTGAAGTGCCAGTGCTGCGACTGCACATTTGTGCAACTCTTAACCCAGCCACATTT 475

Qy   3793 cttccagacaatgaagaaaagataraayataactgtcaacaartaatttctcaaacctat 3852

Db    476 CTTCCAGACAATGAAGAAAAGATAGAACATAACTGTCAACAAGTAATTGCTCAAACCTAT 535

Qy   3853 gccactcgaggggaccttytagargttccyttgactgatccygaccttcaacttgtatac 3912

Db    536 GCTGCTCGAGGGGACCTTCTAGAGGTTCCCTTGACTGATCCCGACC-TCAACTTGTATAC 594

Qy   3913 tgatggaagttcctttgtagaaaaaggacttcgaaaagyggggtatgcagtggtcagtga 3972

Db    595 TGATGGAAGTTCCTTGGCAGAAAAAGGACTTTGAAAAGCGGGGTATGCAGTGATCAGTGA 654

Qy   3973 taatggaatayttgaaagtaatcccctcactccaggaactagtgctyagctrgcagaact 4032

Db    655 TAATGGAATACTTGAAAGTAATCGCCTCACTCCAGGAACTAGTGCTCACCTGGCAGAACT 714

Qy   4033 aatagccytcaytkgggcactagaattaggagaagraaaaagggyaaatatatatacaga 4092

Db    715 AATAGCCCTCACTTGGGCACTAGAATTAGGAGAAGGAAAAAGGGTAAATATATATTCAGA 774

Qy   4093 ctctrartatgctyacctagtcntccatgcccatgmrgcaatatgsaragaaagggaatt 4152

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Qy   4153 cctaacttcygagrgaacacctatcamacatca-ggaagccattaggarattattaytgg 4211

Db    835 CCTAACTTCTGAGGGAACACCTATCAACCATCAGGGAAGCCATTAGGAGATTATTATTGG 894

Qy   4212 cwgtacagaaacctaragaggtggmagtcttacactgcyggggtcatcanaaaggaaagr 4271

Db    895 CTGTACAGAAACCTAAAGAGGTGGCAGTCTTACACTGCCAGGGTCATCAGGAAGAAGAGG 954

Qy   4272 aaagggaaatasaagrgaaytgccaagcakatattgaagcmaaaagagctgcaaggcagg 4331

Db    955 AAAGGGAAATAGAAGGCAATCGCCAAGCGGATATTGAAGCAAAAAAAGCCGCAAGGCAGG 1014

Qy   4332 accctccattagaaatgcttattaaacttcccttagtatagggtaatcccttccgggaaa 4391

Db   1015 ACTCTCCATTAGAAATGCTTATAGAAGGACCCCTAGTATGGGGTAATCCCCTCTGGGAAA 1074

Qy   4392 ccaagccccagtactcagcaggagaaacagaatggggaacctcacgagg---cagttttc 4448
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